

**Amendments to the Specification**

Please replace the Table 3 on page 106 with the replacement Table 3 on the following pages:

Table 3

Mutation	Exon	Exon size	Pop Freq	Location	Sequence Around Mutation Site (SEQ. ID. Nos. 128-191)	PRIMERS	Amp Sz.
297-3 C>T	2	109	Manchester	Sub C>T + 3 Exon 3	CTTTTTATTCC TTTTG(C>T)AGAG	787/788	297
R75Q	3	109	Manchester	Substitute G>A at 60	AATGGGATAGA TAATGCCCTT CGGC(G>A)ATGTT TTTTGTGGA	787/788	297
300 del A	3	109	Manchester	Delete A at 4	ATTCTTTGC AGAGAA TGCG ATAGAGAGCT GGCT	787/788	297
E60X	3	109	Manchester	Substitute G>T at 14	GAATGGGATA GA (G>T) AGCTGGC	787/788	297
L88S	3	109	Manchester	Substitute T>C at 99	CTATGGAAATC TTTT(T>C) ATATT TAGGGGTAAG	787/788	297
G86E	3	109	0.70%	Substitute G>A at 90	TTATATTTAG TTATGTTCTA TG(G>A)AATCTTT CGCGATTAT	787/788	297
R117H	4	216	0.80%	Substitute G>A at 77	AACAAGGAGG AAC(G>A)CTCTAT CGCGATTAT	851/769	381
R117C	4	216	rare	Substitute C>T at 76	AACAAGGAGG AAC(C>t)GCTCTAT CGCGATTAT	851/769	381
Y122X	4	216	0.30%	Substitute T>A at 93	TATCGCGATT TAT(T>A)CTAGGCA TAGGCTTATG	851/769	381
1148T	4	216	F <sub>r</sub> Can (10%)	Substitute T>C at 170	GGCCTTCATC ACA(T>C)TGGAAAT GCAGATGAGA	851/769	381
621+1G>T	4	216	1.30%	Sub G>T after last base	GATTATAAG AAG(G>t)TAATAAC TTCCCTTGAC	851/769	381
711+1G>T	5	90	0.90%	Sub G>T after last base	CAAATTGAT GAA(G>t)TATGTA CCTATTGATT	887/888	289
L206W	6a	164	F <sub>r</sub> Can (10%)	Substitute T>G at 38	TGGATGGCTC CTT(T>G)GCAAGT GGCACTCCCTC	934/935	331
1138 ins G	7	247	Manchester	Insert G at 137	AATCATCCTC CGGAAAGATA TTCACCACCA TCT	789/790	404
1154 ins TC	7	247	Manchester	Insert TC at 153	TATTCAACCAC CATCTCtcAT TCTGCATTGTT	789/790	404

Mutation	Exon	Exon size	Pop Freq	Location	Sequence Around Mutation Site (SEQ. ID. Nos. 128-191)	PRIMERS	Amp Sz.
1161 del C	7	247	Manchester	Delete C at 160	CCACCATCTC ATTCTGcATT CTTCTGGCA TG	789/790	404
R334W	7	247	0.40%	Substitute C>T at 131	AAGGAATCAT CCTC(C>T)GGAAA ATATTCACTTA	789/790	404
R347H	7	247	0.10%	Substitute G>A at 171	CTGCATTGTT CTGC(G>A)CATGG CGGTCACTCG	789/790	404
R347L	7	247	rare	Substitute G>T at 171	CTGCATTGTT CTGC(G>T)CATGG CGGTCACTCG	789/790	404
R347P	7	247	0.50%	Substitute G>C at 171	CTGCATTGTT CTGC(G>c)CATGG CGGTCACTCG	789/790	404
1078 del T	7	247	1.10%	Delete T at 77	CTTCTCTCA GGTTCTTGT GGTGTTTTA TC	789/790	404
1248 + 1 G>A	7	247	Manchester	Sub G>A1 after Exon 7	AAACAAAATA CAG(G>A)TAATGT ACCATAATG	789/790	404
A455E	9	183	0.40%	Substitute C>A at 155	AGGACAGTTG TTGG(c>a)GGTTG CTGGATCCA	891/892	386
G480C	10	192	rare	Substitute G>T at 46	GGAGGCCCTGA CAG(G>T)GTAAAA TTAAGGCACA	760/850	304
O493X	10	192	0.30%	Substitute C>T at 85	TCATTTCTGTT CT(C>T)AGTTTTC CTGGATTAT	760/850	304
D11507	10	192	0.50%	Delete 126, 127, 128	ATTAAGAAA ATATcatCTT TGGTGTCTCC TATG	760/850	304
F508C	10	192	rare	Substitute T>G at 131	TAAAGAAAAT ATCATCT(T>g)TG GTGTTCTCA	760/850	304
DF508	10	192	67.20%	Delete 129, 130, 131	ATTAAGAAA ATATCATCTG GTGTTCTCA TG	760/850	304
V520F	10	192	0.20%	Substitute G>T at 166	TAGATACAGA AGC(G>T)TCATCA AAGCATGCC	760/850	304
1717-1G>A	10	95	1.10%	Sub G>A at +1 Ex11	TATTTTTGGT AATA(G>a)GACAT CTCCAAGTTT	762/763	233
G542X	11	95	3.40%	Substitute G>T at 40	ACAATATAGT TCCT(G>T)GAGAA GGTGGAAAT	762/762	233
S549N	11	95	rare	Substitute G>A at 62	AGGTGGAAATC ACACCTGA(G>A)TG GAGGTCAAACG	762/763	233

Mutation	Exon	Exon size	Pop Freq	Location	Sequence Around Mutation Site (SEQ. ID. Nos. 128-191)	PRIMERS	Amp Sz.
S549I	11	95	rare	Substitute G>T at 62	AGGTGAATCA CACTGA(G>T)TGG AGGTCAAACG	762/763	233
S549R (A>C)	11	95	rare	Substitute A>C at 61	AGGTGGAAATC ACACCTG(A>c)GTG GAGGTCAAACG	762/763	233
S549R (T>G)	11	95	0.30%	Substitute T>G at 63	AGGTGGAAATC ACACTGAG(T>G)G GAGGTCAAACG	762/763	233
G551D	11	95	2.40%	Substitute G>A at 88	ATCACACCTGA GTGGAG(G>A)TCA ACGAGGCAAAGA	762/763	233
G551S	11	95	rare	Substitute G>A at 67	ATCACACCTGA GTGGAG(G>A)GTCA ACGAGGCAAAGA	762/763	233
O552X	11	95	rare	Substitute C>T at 70	ACACTGAGTG GAGGT(C>T)AACG AGCAAGAAATT	762/763	233
R522Q	11	95	rare	Substitute G>A at 74	TGAGTGGAGG TCAAC(G>A)AGCA AGAATTCT	762/763	233
R563X	11	95	1.30%	Substitute C>T at 73	TGAGTGGAGG TCAA(C>t)GAGCA AGAATTCTTT	762/763	233
A559T	11	95	rare	Substitute G>A at 91	GCAAGAATTCTTAA(G>A)CAAG GTGAATAAAC	762/763	233
R560T	11	95	0.40%	Substitute G>C at 95	ATTTCTTTAG CAA(G>C)GTGAAT AACTAA	762/763	233
R560K	11	95	rare	Substitute G>A at 95	GAATTTCTTT AGCAA(G>A)GTGA ATAACTAA	762/763	233
1898 + 1G>A	12	95	0.90%	Sub G>A after last Ex12	GAAATATTTG AAAAG(G>A)TATGT TCTTTGAAT	931/932	299
D648V	13	724	Nst Am (63%)	Substitute A>T at 177	AACTCATGGG ATGTG(A>T)TTCT TTCGACCAAT	955/884	360
2184 del A	13	724	0.70%	Delete A at 286	GACGAAAACAA AAAAaCAATC TTTTAAACAG AC	955/884	360
2184 ins A	13	724	rare	Insert A after 286	GACAGAAAACA AAAAaCAA TCCTTTAAAG CGAC	955/884	360
2789+5G>A	14b	38	1.10%	Sub G>A 5 one after last	CTCCCTGGAA AGTGA(G>A)TATT CCATGTCCTA	885/886	374
3272-26A>G	17a	228	rare	Sub A>G 26 before 17b	TTTATGTTAT TTGCA(A>G)TGTG TTCTATGGAA A	782/901	414

Mutation	Exon	Exon size	Pop Freq	Location	Sequence Around Mutation Site (SEQ. ID. Nos. 128-191)	PRIMERS	Amp Sz.
3272-93T>C	17a	228	rare	Sub T>C 93 before 17b	ATTTGTGATA TGATTA(T>C)TCT AATTAGTCT TT	782/901	414
R1066C	17b	228	rare	Substitute C>T at 57	AGGACTATGG ACACCTT(C>T)GTG CCTTCGGACG GC	782/901	414
L1077P	17b	228	rare	Substitute T>C at 91	TTACTTTGAA ACTC(T>C)GTTCC ACAAAGCTC	782/901	414
Y1092X	17b	228	0.50%	Substitute C>A at 137	CCAACCTGGTT CTTGTA(C>A)CTG TCAACACTGC G	782/901	414
M1101K	17b	228	Mut (65%)	Substitute T>A at 163	TGCGCTGGTT CCAAA(T>A)GAGA ATAGAAATGA T	782/901	414
R1152X	19	249	0.90%	Substitute C>T at 16	ATGCCATCTG TGAGC(C>T)GAGT CTTAAAGTTC	784/785	356
3659 del C	19	249	0.80%	Delete C at 59	AAGGTAAACC TACCAAAGTCA ACCAAACCAT ACA	784/785	356
3849 + 4 A>G	19	249	1.00%	Sub A>G 4 after last base	TCCTGGCCAG AGGGTG(A>G)GAT TTGAACACT	784/785	356
3849 10kb	19	10kb	1.40%	Sub C>T EcoR1 Fragment	ATAAAATGG(C>T) GAGTAAGACA	792/791	450
W1282R	20	156	rare	Substitute T>C at 127	AATAACTTTG CAACAG(T>C)GGA GAAAAGCCCTT T	764/786	351
W1282X	20	156	2.10%	Substitute G>A at 129	AATAACTTTG CAACAGTG(G>A)A GAAAAGCCCTT	764/786	351
3905 ins T	20	156	2.10%	Insert T at 58	CTTTGTTATC AGCTTTTTG AGACTACTGA ACAC	764/786	351
4005 + 1 G>A	20	156	Manchester	Sub G>A after Exon 20	AGTGATACCA CAG(G>A)TGAGCA AAAGGACTT	764/786	351
N1303K	21	90	1.80%	Substitute C>G at 36	CATTTAGAAA AAA(C>G)TTGGAT CCCTATGAAC	756/793	396
N1303H	21	90	rare	Substitute A>C at 34	CATTTAGAAA A(A>C)ACTTGGAT CCCTATGAAC		